

GenCore version 4.5									
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<b>protein - protein search, using sw model</b>									
<b>title:</b> US-09-719-748-2_COPY_13_275									
<b>sequence:</b> May 18, 2002, 05:12:35 ; Search time 42.56 Seconds									
<b>perfect score:</b> (without alignments)									
<b>reached:</b> 239.268 Million cell updates/sec									
<b>scoring table:</b> US-09-719-748-2_COPY_13_275									
<b>BLOSUM62</b>									
<b>Gapext 10.0 , Gapext 0.5</b>									
<b>searched:</b> 105224 seqs, 38719550 residues									
<b>Minimum DB seq length:</b> 0									
<b>Maximum DB seq length:</b> 200000000									
<b>post-processing:</b> Minimum Match 0%									
<b>Maximum Match</b> 100%									
<b>Listing first 45 summaries</b>									
<b>database :</b> SwissProt_40;*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
<b>SUMMARIES</b>									
<b>result</b>									
No.	Score	Query Length	DB ID	Description	RN	RPT;	1431 AA.	ALIGNMENTS	
1	1124	83.7	1431	DARK_HUMAN	1	DARK_HUMAN	STANDARD;	REVIEWS TO 164-171.	
2	653.5	87.7	1176	1 KMUS_BOVIN	AC	P53355;	01-OCT-1996 (Rel. 34. Created)	RA Feinstein E.;	
3	647.5	48.2	1906	1 KMUS_CHICK	DT	01-NOV-1997 (Rel. 35. Last sequence update)	16-OCT-2001 (Rel. 40. Last annotation update)	DT	
4	642.5	47.8	1914	1 KMUS_HUMAN	DE	Death-associated protein kinase 1 (EC 2.7.1.-) (DAPK kinase 1).	DAPK1 OR DAPK.	DE	
5	639	47.5	414	1 S17A_RABBIT	GS	Homo sapiens (Human)	homo sapiens	GS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
6	638	47.5	1147	1 KMUS_RABBIT	OC	Mammalia; Buteraria; Primates; Catarhini; Hominidae; Homo.	NCBI_TaxID=9606;	OC	
7	635.5	47.4	372	1 S17B_RHUMAN	RN	[1]	SEQUENCE FROM N.A.	RN	
8	625	46.5	438	1 KMUS_SHEEP	RX	Medline=95129831; PubMed=7828849;	Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;	RX	
9	611.5	45.5	607	1 KMUC_RABBIT	RJ	"Identification of a novel serine/threonine kinase and a novel 15-kD protein as potential mediators of the gamma interferon-induced cell death."	"Identification of a novel serine/threonine kinase and a novel 15-kD protein as potential mediators of the gamma interferon-induced cell death."	RJ Genes Dev. 9:15-30(1995).	
10	571.5	42.6	609	1 KMUC_RAT	RP	[2]	RN	RP REVISIONS TO 164-171.	
11	530.5	39.5	295	1 KMUC_DICTDI	RA	Reinstein E.;	Submittted (APR-1997) to the EMBL/GenBank/DBJ databases.	RA Feinstein E.;	
12	509	37.9	473	1 KCC4_HUMAN	RL	- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL DEATH.	- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL DEATH.	RL Submittted (APR-1997) to the EMBL/GenBank/DBJ databases.	
13	509	37.9	474	1 KCC4_RAT	CC	- PTM: AUTOPHOSPHORYLATED.	- PTM: AUTOPHOSPHORYLATED.	CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.	
14	505	37.6	469	1 KCC4_MOUSE	CC	- SIMILARITY: CONTAINS 1 DEATH DOMAIN.	- SIMILARITY: CONTAINS 1 DEATH DOMAIN.	CC - SIMILARITY: CONTAINS 1 DEATH DOMAIN.	
15	500	37.2	3038	1 TRIO_HUMAN	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcements or send an email to license@isi-sib.ch).	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcements or send an email to license@isi-sib.ch).	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcements or send an email to license@isi-sib.ch).	
16	495	36.9	533	1 KCCD_RAT	CC	the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcements or send an email to license@isi-sib.ch).	the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcements or send an email to license@isi-sib.ch).	CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announcements or send an email to license@isi-sib.ch).	
17	488	36.3	499	1 KCCD_HUMAN	DR	EMBL: X76104; CAA53712.1; -.	EMBL: X76104; CAA53712.1; -.	DR EMBL: X76104; CAA53712.1; -.	
18	486	36.1	370	1 KCCI_HUMAN	DR	HSSP: 063450; IA06.	HSSP: 063450; IA06.	DR HSSP: 063450; IA06.	
19	485	36.1	374	1 KCCI_RAT	DR	NM: 600811; -.	NM: 600811; -.	DR NM: 600811; -.	
20	483.5	36.0	424	1 KPSH_HUMAN	DR	Inter-Pro; IPR002110; ANK.	Inter-Pro; IPR002110; ANK.	DR Inter-Pro; IPR002110; ANK.	
21	483	36.0	542	1 CDP3_ORYSA	DR	SMART; SM00248; ANK; 7.	SMART; SM00248; ANK; 7.	DR SMART; SM00248; ANK; 7.	
22	480	35.7	533	1 CDP2_ORYSA	DR	Inter-Pro; IPR000719; Euk_Pkinase.	Inter-Pro; IPR000719; Euk_Pkinase.	DR Inter-Pro; IPR000719; Euk_Pkinase.	
23	479.5	35.7	740	1 DCK1_HUMAN	DR	Inter-Pro; IPR002290; Ser_thr_Pkinase.	Inter-Pro; IPR002290; Ser_thr_Pkinase.	DR Inter-Pro; IPR002290; Ser_thr_Pkinase.	
24	478.5	35.6	433	1 DCK1_RAT	DR	PFam: PF00023; ank; 8.	PFam: PF00023; ank; 8.	DR PFam: PF00023; ank; 8.	
25	478.5	35.6	756	1 DCK1_MOUSE	DR	PFam: PF00331; death; 1.	PFam: PF00331; death; 1.	DR PFam: PF00331; death; 1.	
26	475	35.4	478	1 KCPA_RAT	DR	PFam: PF00069; Pkinase; 1.	PFam: PF00069; Pkinase; 1.	DR PFam: PF00069; Pkinase; 1.	
27	475	35.4	424	1 KCPA_MOUSE	DR	SMART; SM00005; DEATH; 1.	SMART; SM00005; DEATH; 1.	DR SMART; SM00005; DEATH; 1.	
28	471	35.1	478	1 KCCA_MOUSE	DR	SMART; SM00220; S_TKC; 1.	SMART; SM00220; S_TKC; 1.	DR SMART; SM00220; S_TKC; 1.	
29	469	34.8	532	1 CDP1_DAICA	DR	PROSITE; PS50088; ANK_REPEAT; 6.	PROSITE; PS50088; ANK_REPEAT; 6.	DR PROSITE; PS50088; ANK_REPEAT; 6.	
30	468	34.8	610	1 CDP1_ARATH	DR	PROSITE; PS500297; ANK REP_REGION; 1.	PROSITE; PS500297; ANK REP_REGION; 1.	DR PROSITE; PS500297; ANK REP_REGION; 1.	
31	464	34.8	534	1 CDP1_ORYSA	DR	PROSITE; PS50017; DEATH_DOMAIN; 1.	PROSITE; PS50017; DEATH_DOMAIN; 1.	DR PROSITE; PS50017; DEATH_DOMAIN; 1.	
32	464	34.4	508	1 CDP1_SOBN	DR			DR	
33	462	34.4	1		DR			DR	



FT	DOMAIN	1171	1176	POLY-GLU.
SQ	SEQUENCE	1176 AA;	128824 MW;	F53DC6D4D42D4B97 CRC64;
Query Match				
Best Local Similarity	48.7%	Score 653.5;	DB 1;	Length 1176;
Matches	128;	Conservative	48;	Mismatches 79;
Indels	9;	Gaps 3;		
Oy	1	YDIGEEGLSGQFAVKKRREKSTGLEYAAFKKRQSRSARRGVSVREEREVSIQLQVL 60		
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :		
	725	YDIEERLGSGKFGQFVERLVEKKGKIWAKKFAYKS-----EKENTROEISIMNCLH 778		
Oy	61	HHWVITLHDVYERTDVHILELVGGELDFLAQE-SLEEBERATSIKQIQLGVNVHL 119		
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :		
Db	779	HPKLVQCVDAFEKANIVMWEVSGGLEFLERIDDEFELTERECIKWMQISBGVEVH 838		
Oy	120	TKKIAHEDLKPPENMLDKNPINPIPHIKLDFGLAHETDGVFKNIFSPFPEVAPETVY 179		
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :		
Db	839	KOGIVHVDLKPENIMCVAKT-GTRIKLIDFGLARRLNAGSKVLFGPPEFPEVINK 896		
Oy	180	EPLGLEADMWSIGVITYLILSGASPFEGDTKQELANTTSVSYDFDEEFSSHTSELADF 239		
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :		
Db	897	EPIGVATDMWSIGVICVILVLSGLSPFMGDNDNETLANVTSATWDFFDEADEFDDAKDF 956		
Oy	240	IRKLKVKEETRKRTIQEALRHFWI 263		
		:   :   :   :   :   :   :   :   :   :   :   :   :   :		
Db	957	ISNLKKDMDKRNLRNCTQCLQHPWL 980		
RESULT 3				
KMLS_CHICK	STANDARD;	PRTR;	1906 AA.	
ID	P11799; P19038;			
DR	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DE	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Myosin light chain kinase, smooth muscle and non-muscle isoforms			
DE	(BC_27.1.117) (MCK) [Contains: Telokin].			
OS	Gallus gallus (Chicken)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OX	NCBI_TAXID=9031;			
RN	SEQUENCE FROM N.A. (MCK-210).			
RP	MEDLINE-96033976; PubMed=7589469;			
RA	Waterson D.M., Collinge M., Lukas T.J., van Eldik L.J., Birukov K.G.,			
RA	Stepanova O.V., Shirinsky V.P.,			
RA	"Multiple gene products are produced from a novel protein kinase			
RT	transcription region."			
RT	FEBS Lett. 373:217-220(1995).			
RN	SEQUENCE FROM N.A. (MCK-108).			
RP	MEDLINE=90192792; PubMed=2315320;			
RA	Olson N.J., Pearson R.B., Needlemen D.S., Hurwitz M.J., Kemp B.B.,			
RA	Means A.R.;			
RT	"Regulatory and structural motifs of chicken gizzard myosin light			
RT	chain kinase.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:2284-2288(1990).			
RN	SEQUENCE OF 649-1906 FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE-Fibroblast;			
RX	MEDLINE=9031738; PubMed=2202734;			
RA	Shoemaker M.O., Lau W., Shattuck R.L., Kwiatkowski A.P.,			
RA	Matrisian P.E., Guerrero-Santos L., Wilson E., Lukas T.J.,			
RA	van Eldik L.J., Waterson D.M.;			
RA	"Use of DNA sequence and mutant analyses and antisense			
RT	oligonucleotides to examine the molecular basis of nonmuscle			
RT	myosin light chain kinase autoinhibition, calmodulin recognition, and			
RT	activity.";			
J. Cell Biol.	111:1107-1125(1990).			
[4]	SEQUENCE OF 1259-1906 FROM N.A.			
SEQUENCE OF 1750-1906 FROM N.A. (TELOKIN)				
RC	MEDLINE=87157587; PubMed=3030394;			
RA	Guerrero V. Jr., Russo M.A., Olson N.J., Putkey J.A., Means A.R.;			
RT	"Domain organization of chicken gizzard myosin light chain kinase deduced from a cloned cDNA.";			
RT	Biochemistry 25:8372-8381(1986).			
RL	[5]			
RP	SEQUENCE OF 1750-1906 FROM N.A. (TELOKIN)			
RC	TISSUE-Gizzard;			
RA	MEDLINE=93073972; PubMed=1444462;			
RA	Yoshitai S., Ikebe M.;			
RA	"Molecular cloning of the chicken gizzard telokin gene and cDNA.";			
RT	Arch. Biochem. Biophys. 295:242-247(1992).			
RL	[6]			
RP	SEQUENCE OF 1750-1906 FROM N.A. (TELOKIN)			
RX	MEDLINE=92236611; PubMed=1373815;			
RA	Collinge M., Matrisian P.E., Zimmer W.E., Shattuck R.L., Lukas T.J.,			
RA	van Eldik L.J., Waterson D.M.;			
CC	"Structure and expression of a calcium-binding protein gene contained			
CC	within a calmodulin-regulated protein kinase gene.";			
RL	Mol. Cell. Biol. 12:2359-2371(1992).			
CC	-I- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin			
CC	light-chain] phosphate.			
CC	-I- FUNCTION: PROSPORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A			
CC	MYOSIN LIGHT CHAIN WHICH LEADS TO THE FORMATION CALMODULIN/			
CC	MICK SIGNAL TRANSDUCTION COMPLEXES WHICH ALLOW SELECTIVE			
CC	C-TERMINAL SECTION WITH NO CATALYTIC ACTIVITY).			
CC	-I- TISSUE SPECIFICITY: TELOKIN IS EXPRESSED IN GIZZARD, HEART, LUNG,			
CC	INTESTINE, AND SKELETAL MUSCLE ALTHOUGH THE LEVELS OF THE			
CC	EXPRESSION IN THE LATTER ARE MUCH LESS THAN THAT IN THE GIZZARD.			
CC	-I- DOMAIN: TELOKIN BINDS CALMODULIN.			
CC	-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	-I- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.			
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CC	or send an email to license@isb-sib.ch).			
EMBL	X52876; CAA37055.1; -			
EMBL	X52876; CAA37057.1; -			
EMBL	X52876; CAA37058.1; -			
EMBL	M31048; AAA9069.1; -			
EMBL	M14953; AAA69964.1; -			
EMBL	M96555; AAA49083.1; -			
EMBL	M8203; AAA6547.1; -			
EMBL	M88284; AAA53768.1; -			
PIR	A25810; A25810.			
PIR	A3709; A3709.			
PIR	S11652; S11652.			
HSSP	P56276; ITRK.			
InterPro	IPR00719; Bok_pk kinase.			
InterPro	IPR00596; FNIII.			
InterPro	IPR00506; Ig_MHC.			
InterPro	IPR03598; Ig_C2.			
InterPro	IPR03600; Ig_Like.			
InterPro	IPR002290; Ser_thr_pk kinase.			
PFam	PF00041; In3; 1.			
PFam	PF00047; Ig; 9.			
DR	Pfam; PF00069; Pkinase; 1.			
DR	SMART; SM00060; FN3; 1.			
DR	SMART; SM00410; Ig_Like; 1.			
DR	SMART; SM00408; IGC2; 8.			
DR	SMART; SM00220; S_TKC; 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			





QY	180	EPGLEADMSLIGVITYVILLSGASPLGLDTKQETLANITSVYDFDEEFSTHTSBLAKDF	239	N---VITLHDVYENRTDVHILEVSGELFD---FLAQKESLSSEBEATSIKQIDGVWYL	118
Db	1636	EPGYATDMWSIGVITYVILLSGASPLGDPKQETLANITSVYDFDEEFSTHTSBLAKDF	1695	:         :         :         :         :         :         :         :	160
QY	240	TRKLKVKEKRKLTQEARHPW	263	:         :         :         :         :         :         :         :	178
Db	1696	ISNLKKDMKNRDLCTQCLQHPW	1719	:         :         :         :         :         :         :         :	219
RESULT	5	S17A_RABBIT	STANDARD;	PRT;	397 AA.
ID	S17A_RABBIT				
AC	09GM0;				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Serine/threonine kinase 17A (EC 2.7.1.-) (DAP kinase-related apoptosis-inducing protein kinase 1) (rDRAK1).				
GN	STK17A OR DRAK1.				
OS	Oryctolagus cuniculus (Rabbit)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX	NCBI_TAXID=9986;				
RN	[1] SEQUENCE FROM N.A.				
RP	TISSUE=osteoclast;				
RX	MEDLINE=21616420; PubMed=11279167;				
RA	Kojima H., Nemoto A., Uemura T., Romma R., Ogura M., Liu Y.-K.; "rDRAK1, a novel kinase related to apoptosis, is strongly expressed in active osteoclasts and induces apoptosis.", J. Biol. Chem. 276:1938-1943(2001).				
RT	-!- FUNCTION: PHOSPHORYLATES THE MOSIN LIGHT CHAIN (MLC) (BY SIMILARITY) AND IS INVOLVED IN OSTEOCLAST APOPTOSIS.				
RL	CC				
CC	-!- SUBCELLULAR LOCATION: Nuclear.				
CC	-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BONE MARROW AND IN LOWER LEVELS IN BRAIN, HEART, LUNG, LIVER AND KIDNEY.				
CC	-!- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).				
CC	-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINESSES.				
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DR	EMBL; AB04195; BAB16111.1; -.				
DR	InterPro: IPR000719; Euk_pk kinase.				
DR	InterPro: IPR002290; Ser_thr_pk kinase.				
DR	InterPro: IPR001245; Tyr_P kinase.				
DR	pfam; PF00069; Pkinase; 1.				
DR	SMART; SM00220; S_TK_C; 1.				
DR	SMART; SM00219; TYRK; 1.				
DR	PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.				
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.				
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.				
KW	Transferase; Serine/threonine protein kinase; ATP-binding;				
KW	Phosphorylation; Nuclear Protein; Apoptosis.				
FT	DOMAIN 44 304 PROTEIN KINASE.				
FT	NP_BIND 50 58 ATP (BY SIMILARITY).				
FT	BINDING 73 73 ATP (BY SIMILARITY).				
SEQUENCE	397 AA;	44462 MW;	589041E10/F50097 CRC64;		
Query Match	47.6%	Score 639; DB 1; Length 397;			
Best Local Similarity	46.0%	Pred. No. 2e-34; Mismatches 67; Indels 12; Gaps 6;			
Matches	122;	Conservative			
QY	4	GEGLGSGQPAVVKCRENRGTYAAFKIKRROSRRGVS-REPIEREVSIILRQLVHH	62	63 N---VITLHDVYENRTDVHILEVSGELFD---FLAQKESLSSEBEATSIKQIDGVWYL	118
Db	47	GRELGRGKFAVVRKCIQDKSGKEFAKFMKR----RKGDCRMELIHEAVL-EAQD	100	:         :         :         :         :         :         :	160
QY	63	YEPGLLEADMWSIGVITYVILLSGASPLGDPKQETLANITSVYDFDEEFSTHTSBLAKDF	239	:         :         :         :         :         :         :	178
Db	101	NPWVNLNREVETSESEMILVLEYAGGEISDQCVDARENEKDVRMLQLEGVPL	160	:         :         :         :         :         :	219
QY	119	HIIKKIAHEDKENTMILDKIPIPHIKLIDFGLAHEIEDGEVERKNIFGTPPEVAPENV	238	:         :         :         :         :         :	238
Db	161	HTDVVHLDPKPNQILLSES-PLGDKIVDFGLSLVIKNSSEELREIMGTPPEVAPENV	219	:         :         :         :         :	279
QY	179	YEPGLLEADMWSIGVITYVILLSGASPLGDPKQETLANITSVYDFDEEFSTHTSBLAKDF	239	:         :         :         :         :	279
Db	220	YDPISMATDMWSIGVITYVMLNGISPLGLDNKQETFLNISOMLISYEEEDTVSEAVD	239	:         :         :         :	279
RESULT	6	S17A_HUMAN	STANDARD;	PRT;	414 AA.
ID	S17A_HUMAN				
AC	09UE5;				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	Serine/threonine kinase 17A (EC 2.7.1.-) (DAP kinase-related apoptosis-inducing protein kinase 1).				
GN	rDRAK1 OR DRAK1.				
OS	Homo sapiens (Human).				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TAXID=9606;				
RN	[1] SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-90.				
RP	J. Biol. Chem. 273:29066-29117(1998).				
RC	TISSUE=Placenta, and Liver;				
RX	MEDLINE=99032259; PubMed=9786912;				
RA	Sanjo H., Kawai T., Akira S.; "rDRAKs, novel serine/threonine kinases related to death-associated protein kinase that trigger apoptosis.", J. Biol. Chem. 273:29066-29117(1998).				
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CC	or send an email to license@isb-sib.ch).				
CC	CC				
CC	-!- FUNCTION: PHOSPHORYLATES THE MOSIN LIGHT CHAIN (MLC) AS AN EXOGENOUS SUBSTRATE AND IS INVOLVED IN APOPTOTIC SIGNALING. THE C-TERMINAL REGION PLAYS AN IMPORTANT ROLE IN KINASE ACTIVITY AND FOR INITIATION OF APOPTOSIS.				
CC	-!- SUBCELLULAR LOCATION: Nuclear.				
CC	-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA, AND IN LOWER LEVELS IN HEART, LUNG, SKELETAL MUSCLE, KIDNEY AND PANCREAS.				
CC	-!- PTM: AUTOPHOSPHORYLATED.				
CC	-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINESSES.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).				
CC	or send an email to license@isb-sib.ch).				
DR	EMBL; AB01142; BA34126.1; -.				
DR	DR				
DR	HSSP; P0518; IPHK.				
DR	MM: 604726; -.				
DR	InterPro: IPR000719; Euk_pk kinase.				
DR	pfam; PF00069; Pkinase; 1.				
DR	SMART; SM00220; S_TK_C; 1.				
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.				
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.				
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.				
DR	InterPro: IPR000719; Ser_thr_pk kinase.				
DR	pfam; PF00069; Pkinase; 1.				
DR	SEQUENCE				
Query Match	47.6%	Score 639; DB 1; Length 397;			
Best Local Similarity	46.0%	Pred. No. 2e-34; Mismatches 67; Indels 12; Gaps 6;			
Matches	122;	Conservative			
QY	4	GEGLGSGQPAVVKCRENRGTYAAFKIKRROSRRGVS-REPIEREVSIILRQLVHH	62	63 N---VITLHDVYENRTDVHILEVSGELFD---FLAQKESLSSEBEATSIKQIDGVWYL	118
Db	47	GRELGRGKFAVVRKCIQDKSGKEFAKFMKR----RKGDCRMELIHEAVL-EAQD	100	:         :         :         :	160



	FT	BINDING	62	62	ATP (BY SIMILARITY)
	FT	MUTAGEN	62	62	K>A: LOSS OF ACTIVITY
	SEQUENCE	372 AA:	42344 MN:	7E69FFAED6DC1FF3 CRC64;	
Db	750	HPKLVQCVDAFEERKANIVMELVSGGELFERIIDEFELTERCICKYMRQISEGEVYH	809		
QY	120	TKKIAHFDFKPEIMLDKNIPHTKLIDGLAHIEDGEVERNIFCPPEFVAPETWY	179		
Db	810	KQGIVHLDKPENIMCVNKT-GTRKLIDGLARLENAGSLVLFGLPFEPVAPETWY	867		
QY	180	EPLGLEADMSIGTYILSGASPFGLGDTKOTELANITSYDDEEFSTELAKDF	239		
Db	868	EPISYATDMWSIGVIVCYLVLGSPFMGDNDNETLANVTSATWDFDEAFDEISDAKDF	927		
QY	240	IRKKLVKETRKRLTQEAIRHPWI	263		
Db	928	INNLKKDMNRDCTQCLQRHPWL	951		
RESULT	8				
ID	S17B_HUMAN	STANDARD;	PRT:	372 AA.	
AC	094768;				
DT	16-OCT-2001 (Rel: 40, Created)				
DT	16-OCT-2001 (Rel: 40, Last sequence update)				
DT	16-OCT-2001 (Rel: 40, Last annotation update)				
DE	Serine/threonine kinase 17B (EC 2.7.1.-) (DAP kinase-related apoptosis-inducing protein kinase 2).				
GN	STK17B OR DRAK2.				
OS	Homo sapiens (Human)				
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiodactyla; Homo.				
NCBI_TAXID=9606;					
OX					
RN	[1] SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-62.				
RP	SEQUENCE FROM PLACENTA, and Liver;				
RX	MEDLINE=99032529; PubMed=9786912;				
RA	Sanjo H., Kawai T., Akira S.;				
RT	"DRAKs", novel serine/threonine kinases related to death-associated protein kinase that trigger apoptosis.				
RT	J. Biol. Chem. 273:29066-29071(1998).				
RL	TISSUE-SPECIFICITY: THE MYOSIN LIGHT CHAIN (MLC) AS AN EXOGENOUS SUBSTRATE AND IS INVOLVED IN APOPTOTIC SIGNALING. THE C-TERMINAL REGION PLAYS AN IMPORTANT ROLE IN KINASE ACTIVITY AND FOR INITIATION OF APOPTOSIS.				
CC	-1- SUBCELLULAR LOCATION: Nuclear.				
CC	-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA, LUNG, PANCREAS AND IN LOWER LEVELS IN HEART, BRAIN, LIVER, SKELETAL MUSCLE AND KIDNEY.				
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.				
CC	-1- FTM: AUTOPHOSPHORYLATED.				
CC	-1- Tissue Specificity: Highly expressed in placenta, lung, pancreas and in lower levels in heart, brain, liver, skeletal muscle and kidney.				
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CC	EMBL: AB011421; BAA34127.1; -.				
DR	HSSP: P00518; IPIK.				
DR	MIM: 604277; - Euk_Pkinase.				
DR	InterPro: IPR000719; Ser-thr_Pkinase.				
DR	InterPro: IPR002290; Sel-thr_Pkinase.				
DR	InterPro: IPR001245; Tyr_Pkinase.				
DR	Pfam: PF00059; Pkinase_1.				
DR	PRINTS: PRO0119; ITRKINASE.				
DR	SMART: SM00210; S_TKC_1.				
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.				
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.				
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.				
DR	Transf erase: Serine/threonine-protein kinase; ATP-binding.				
KW	Phosphorylation; Nuclear protein; Apoptosis.				
KW	Protein kinase.				
FT	DOMAIN: 308 311 POLY-SR.				
FT	DOMAIN: 308 311 POLY-SR.				
NP_BIND	39 47 ATP (BY SIMILARITY).				
RESULT	9				
ID	KM15_SHEEP	STANDARD;	PRT:	438 AA.	
AC	002827;				
DT	15-JUL-1998 (Rel: 36, Created)				
DT	15-JUL-1998 (Rel: 36, Last sequence update)				
DT	16-OCT-2001 (Rel: 40, Last annotation update)				
DE	Myosin light chain kinase, smooth muscle (EC 2.7.1.117) (MLCK)				
DE	[Contains: Telokin] (Fragment).				
DE	MYLK.				
OS	Ovis aries (Sheep); Chordata; Craniata; Vertebrata; Pecora; Bovidae; Mammalia; Eutheria; Caprinae; Ovis.				
OC	Bovidae; Caprinae; Ovis.				
NCBI_TAXID=9940;					
OX					
RN	[1] SEQUENCE FROM N.A., PubMed=8569750;				
RP	SEQUENCE FROM PLACENTA, and Partial sequence of pregnant sheep myometrium				
RX	MEDLINE=96139339; PubMed=8569750;				
RA	Pato M.D., Kerc E., Lye S.J.; "Phosphorylation and partial sequence of pregnant sheep myometrium light chain kinase." Mol. Cell. Biochem. 149:59-65(1995).				
RT	-1- FUNCTION: PHOSPHORYATES A SPECIFIC SERINE IN THE N-TERMINUS OF A MOSIN LIGHT CHAIN.				
CC	-1- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin light-chain] phosphate.				
CC	-1- DOMAIN: TELOKIN BINDS CALMODULIN.				
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.				
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.				
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CC	EMBL: S80867; ARB0715.2; -.				
DR	HSSP: P56276; ITLK.				
DR	InterPro: IPR00719; ENK_Pkinase.				
DR	InterPro: IPR003006; Ig_MHC.				
DR	InterPro: IPR003598; Ig_c2.				

DR	InterPro; IPR002290; Ser-thr_pk kinase.	RP	SEQUENCE OF 295-603.
Pfam	PF00049; pkinase; 1.	RX	MEDLINE-86104095; PubMed-3841288;
SMART	SM00408; IgC2; 1.	RA	Takino K., Blumenthal D.K., Edelman A.M., Walsh K.A., Krebs E.G.,
SMART	SM00220; S_TKc; 1.	RA	Titan K.;
PROSITE	PS00107; PROTEIN_KINASE_ATP; PARTIAL.	RT	"Amino acid sequence of an active fragment of rabbit skeletal muscle
PROSITE	PS00108; PROTEIN_KINASE_ST; 1.	RT	myosin light chain kinase;"
PROSITE	PS00111; PROTEIN_KINASE_DOM; 1.	RL	Biochemistry 24: 6028-6037(1985).
KW	transf erase; Serine/threonine-protein kinase; Calmodulin-binding;	RN	[4]
ATP-binding; Phosphorylation; Immunoglobulin domain.		RP	STRUCTURE BY NMR OF 577-602.
NON_TER	1	RX	MEDLINE-92263094; PubMed-1585175;
FT	<1	RA	Ikura M., Clore G.M., Gronenborn A.M., Zhu G., Klee C.B., Bax A.;
DOMAIN	241	RT	"Solution structure of a calmodulin-target peptide complex by
FT	296	RT	multidimensional NMR";
DOMAIN	345	RL	Science 256: 632-638(1992).
FT	413	CC	-i- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
BINDING	15	CC	MYOSIN LIGHT CHAIN.
ACT_SITE	107	CC	-i- CATALYTIC ACTIVITY: ATP + [myosin light-chain] = ADP + [myosin
FT	107	CC	light-chain phosphate].
DOMAIN	283	CC	-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
FT	438	CC	-----
SEQUENCE	438 AA; 49503 MW; 77A0284885A10B51 CRC64;	CC	-----
Query Match	45.5%; Score 611.5; DB 1; Length 438;.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
Best Local Similarity	48.2%; Pred. No. 1.3e-32;.	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
Matches	118; Conservative	CC	the European Bioinformatics Institute. There are no restrictions on its
	46; Mismatches	CC	use by non-profit institutions as long as its content is in no way
	72; Indels	CC	modified and this statement is not removed. Usage by and for commercial
OY	20 EKSTGLEPAKIKRKKRSRASRRGVSREEVSLRQLVHNVITLHDVNRDQWH	CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> )
DB	5 VLEIVSGGELFFERIIDEFELTRECIRYMKOISSEGVEYIHKOGIVHLQDKPENIMCVN	CC	or send an email to license@isb-sib.ch).
OY	139 NIPIPHKLIDGLAHIEDGEPEFKNFGTPEEVAPEVINYPLGLADMSIGVITYL	CC	-----
DB	119 T-GTRRIKLDGLGALARLNAGSLKVLFGTGPESRVAPEVINYPIGYANDMSIGVICYL	CC	-----
OY	199 LSGASPLGDUQTETLANTTSYDFLDEFFSHTSDEAKDFTRKLQKRETAKLQAL	CC	-----
DB	177 VSGLSPPMGNDNETLANTVTSATWDFFDDEAFDEISDDAKDFISNLKKCIKRNLCQCL	CC	-----
OY	259 RHPWI 263	CC	-----
DB	237 QHPWL 241	CC	-----
RESULT	10	CC	-----
ID	KMLC_RABBIT	CC	-----
AC	P07313; P0713;	CC	-----
DT	01-APR-1990 (Rel. 14, last sequence update)	CC	-----
DT	16-OCT-2001 (Rel. 40, last annotation update)	CC	-----
DE	Myosin light chain kinase, skeletal muscle (EC 2.7.1.117) (MLCK).	CC	-----
OS	Oryctolagus cuniculus (Rabbit).	CC	-----
OC	Bukarrotta; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;	CC	-----
OX	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	CC	-----
NCBItaxId	9986;	CC	-----
RN	[1]	CC	-----
SEQUENCE FROM N_A.		CC	-----
RX	MEDLINE-90110242; Published=1688558;	CC	-----
RP	Herring B.P., Stull J.T., Gallagher P.J.;	CC	-----
RT	"Domain characterization of rabbit skeletal muscle myosin light chain	CC	-----
J. Biol. Chem.	265:1724-1730(1990).	CC	-----
RN	[2]	CC	-----
RP	SEQUENCE OF 1-603.	CC	-----
RX	MEDLINE-8701105; Published=3542042;	CC	-----
RA	Takio K., Blumenthal D.K., Walsh K.A., Titani K., Krebs E.G.;	CC	-----
RT	"Amino acid sequence of rabbit skeletal muscle myosin light chain	CC	-----
J. Biol. Chem.	25:8049-8057(1986).	CC	-----
RN	[3]	CC	-----
Query Match	42.6%; Score 571.5; DB 1; Length 607;.	CC	-----
Best Local Similarity	43.1%; Pred. No. 6.9e-30;.	CC	-----
Matches	112; Conservative	CC	-----
	54; Mismatches	CC	-----
	85; Indels	CC	-----
RN	SEQUENCE FROM N_A.	CC	-----
QY	5 EELGGQQFAIVKKCIREKSTGLEYAKFKIKRQQSRRGVSREEVSLRQLVHNV	CC	-----
DB	300 EALGGQQFAIVKKCIREKSTGLEYAKFKIKRQQSRRGVSREEVSLRQLVHNV	CC	-----
QY	65 ITLHWYENRHDVWHILEVSGGELFFLAQKE-SLSEEAEATSFHQIQLDGYNLTKKI	CC	-----
DB	354 IOLYVAIETPHEIVLFMEYEGGEPEVIRVEDYHTEVDMVFWRCIDCILFLMHRM	CC	-----
QY	124 AHFDLKPENTMLDKNIPHIKLDFGLAHEIEGVFKNFGPEFVAPEVINYPLG	CC	-----
DB	414 LHLDPKENTLCVNTGHL-VKIDFLGLARRYNNNEKLVNFQGPFLSPVVNVDQI	CC	-----
QY	184 LEADMWSIGVITYLILSAGSPLFLGQTKQETLANTTSVSYDFEDEFSTSBLAKDFIRK	CC	-----



DR	InterPro; IPR002290; Ser_thr_pk kinase.
DR	Pfam; PF00069; kinase_1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP_1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST_1.
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; phosphorylation.
FT	PROTEIN_KINASE.
FT	PROTEIN_KINASE_DOMAIN.
FT	NP_BIND 264 295 AUTOINHIBITORY_DOMAIN.
FT	ATP (BY SIMILARITY).
FT	ATP (BY SIMILARITY).
FT	ACT_SITE 130 130 BY SIMILARITY.
SEQ	SEQUENCE 295 AA: 33406 MW: 546CABED8FECDB CRC64;
Query Match	39.5%; Score 530.5; DB 1; Length 295;
Best Local Similarity	43.5%; Pred. No. 1.3e-27;
Matches	115; Conservative 41; Mismatches 101; Indels 7; Gaps 3;
OY	1 YDIGEELGSGQFAIVKCKREKSTGGLEYAAFKKKRQRQSRRGVSREE-IEREVSIIRQV 59
DB	8 YFKEKEELGRGAISIVVLYGENKPKTKORYAIVKINK----SELGKDYERKLKHEVIDLKKV 62
OY	60 LHNHVTLDHVENRTDVHLEVLNSGELFLAQKESLSREATSFIQTLGDNVNLH 119
DB	63 NHPNITALKEELDPTEKYLWHLVLYGEFLPKIVEGSYSADAANLUKKIVSAYVLH 122
OY	120 TTKIAHFDLKPNIMLLDKNIPHIKLUDEGLAHETEDGVSPKNITGTPPERVAPETVY 179
DB	123 GLNIVHDKLPENNLLSKENHL-EVALADFGSLKIQGQLWMTAGCTPSVPAEVLNA 181
OY	180 EPLGLEADMWSIGVITYVILLSGASPELDTKOTBLANITSVYDDEFERFSTISELKDF 239
DB	182 TGYDKEYDMWSIGVITYILLCCFPFPYGDVPEIFEQIMEANEYEPSEYWGTSKEADF 241
OY	240 IRKLLVWVDSKRUNATNALNHPWL 263
DB	242 IKRLLVWVDSKRUNATNALNHPWL 265
RESULT	13
KCC4_HUMAN	
ID	KCC4_HUMAN STANDARD; PRT: 473 AA.
AC	Q16566; 01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Calcium/calmodulin-dependent protein kinase type IV catalytic chain (EC 2.7.1.123) (CaM Kinase-GR) (CaMK IV) [Contains: Calsperrin].
GN	CAMK4.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrini; Hominoidea; Homo.
OX	NCBI_TAXID:9606; NCBI_TAXON:9606;
RN	[1] SEQUENCE FROM N.A.
RK	MDLINV*94375404; Pubmed=8089075;
RA	Kitani T., Okuno S., Fujisawa H.;
RC	"CDNA cloning and expression of human calmodulin-dependent protein kinase IV," J. Biochem. 115:637-640(1994).
RT	TISSUE=Cerebellum, and Thymus;
RT	MDLINV*94252566; Published=8394751;
RA	Bland M.M., Monroe R.S., Olmstede C.A.;
RT	"The cDNA sequence and characterization of the Ca2+/calmodulin-dependent protein kinase-Gr from human brain and thymus," Gene 142:191-197(1994).
RI	[3] SEQUENCE FROM N.A.
RP	
Query Match	37.9%; Score 509; DB 1; Length 473;
Best Local Similarity	40.7%; Pred. No. 5.4e-26;
Matches	109; Conservative 49; Mismatches 92; Indels 18; Gaps 5;
OY	1 YDIGEELGSGQFAIVKCKREKSTGGLEYAAFKKKRQRQSRRGVSREE-IEREVSIIRQV 60
DB	46 FEVESEGRGATSTVYRCKGKTPQYALVKLH----VDKKVTRTEGVLLRLS 97
OY	61 HHNVTLDHVENRTDVHLEVLNSGELFLAQKESLSREATSFIQTLGDNVNLH 120
DB	98 HPNTIKLKIEFTEIISLVELTIGGELFDRIVEKGYSERDADAVQILEAVAYLHR 157
OY	121 KKLIAHFDLKPNIMLLDKNIPHIKLUDEGLAHETEDGVSPKNITGTPPERVAPETVY 178
DB	158 NGTIVHDLKPKENLLYA---TPAPDAPLKTADFGLSKIVHQVLMKTVGTPGCAPEIL 214
OY	179 YEPGLEADMWSIGVITYVILLSGASPEL--GDTKQETLANTISVSYDDEFSHTTEL 235
DB	215 GCAYGPVNDMSIGVITYILLCGPFEPYDGR-QFMFRILNEYCEYPTSPWDEVSLN 272
OY	236 AKDFTIRKLVKETRKRLTQEARLHPWI 263
DB	273 AKDLVRLKLVLDPPKKRRTTFOALOHPWV 300

us-09-719-748-2\_copy\_13\_275.rsp

RESULT 14  
 KC4\_RAT STANDARD; PRT; 474 AA.  
 ID KCC4\_RAT  
 AC P13234;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-APR-1993 (Rel. 25, Last annotation update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Calcium/calmodulin-dependent protein kinase type IV catalytic chain  
 (EC 2.7.1.123) (CAM kinase-GR) (Camk IV) [Contains: Calspermin].  
 GN CAMK4.  
 OS Rattus norvegicus (rat).  
 OC Mammalia; Metazoa; Chordata; Craniata; vertebrata; Buteleostomi;  
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TAXID=10116;  
 RN [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=91208548; PubMed=1648230;  
 RA Ohnsteide C.R., Bland M.M., Merrill B.M., Sabyoun N.;  
 RT Relationship of genes encoding Ca<sup>2+</sup>/calmodulin-dependent protein  
 kinase Gr and calspermin: a gene within a gene.;  
 RT PROC. Natl. Acad. Sci. U.S.A. 88(8):5784-5788(1991).  
 RN [2] SEQUENCE FROM N.A.  
 RX MEDLINE=91304387; PubMed=1649385;  
 RA Means A.R., Cruzalegui F., Lemaguereese B., Needleman D.S.,  
 RA Slaughter G.R., Ono T.;  
 RT Ca<sup>2+</sup>/calmodulin-dependent protein kinase and a male germ  
 cell-specific calmodulin-binding protein are derived from the same  
 RT gene.;  
 RL Cell. Biol. 11:3960-3971(1991).  
 RN [3] SEQUENCE OF 250-474 FROM N.A.  
 RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;  
 RA Ohnsteide C.-A., Jenson K.F., Sabyoun N.;  
 RT "Ca<sup>2+</sup>/calmodulin-dependent protein kinase enriched in cerebellar  
 granule cells. Identification of a novel neuronal  
 calmodulin-dependent protein kinase.";  
 RL J. Biol. Chem. 264:5866-5875(1989).  
 RN [4] SEQUENCE OF 306-474 FROM N.A., AND SEQUENCE OF 335-361.  
 RX MEDLINE=8912327; PubMed=2914893;  
 RA Ono T., Slaughter G.R., Cook R.G., Means A.R.;  
 RT "Molecular cloning sequence and distribution of rat calspermin, a  
 high affinity calmodulin-binding protein.";  
 RT J. Biol. Chem. 264:2051-2087(1989).  
 RL STRAIN=SPRAGUE-DAWLEY;  
 CC ENRICHED IN CEREBELLAR GRANULE CELLS.  
 CC ENRICHED IN HEAT-STABLE, ACIDIC, CALMODULIN-BINDING  
 CC FUNCTION: CALSPEMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING  
 CC PROTEIN.  
 CC -I- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE  
 CC TYPE IV CATALYTIC CHAIN AND CALSPEMIN ARE OBTAINED BY ALTERNATIVE  
 CC SPlicing.  
 CC -I- TISSUE SPECIFICITY: CALSPEMIN IS PREDOMINANTLY FOUND IN MAMMALIAN  
 CC TESTIS AND BRAIN.  
 CC -I- PWM: THE N-TERMINAL OF CALSPEMIN IS BLOCKED.  
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC CAMK SUBFAMILY.

RESULT 15  
 KC4\_MOUSE STANDARD; PRT; 469 AA.  
 ID KCC4\_MOUSE  
 AC P08114; Q61381;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-APR-1993 (Rel. 25, Last annotation update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Calcium/calmodulin-dependent protein kinase type IV catalytic chain  
 (EC 2.7.1.123) (CAM kinase-GR) (Camk IV) [Contains: Calspermin].  
 GN CAMK4.  
 OS Mus musculus (Mouse);  
 OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TAXID=10890;  
 RN [1] SEQUENCE FROM N.A.  
 RX STRAIN=BALBC; TISSUE=Brain;  
 RA MEDLINE=9172388; PubMed=1893997;  
 RA Jones D.A., Glad J., Wilson-Shaw D., Hahn W.E., Sikela J.M.;  
 RT "cDNA sequence and differential expression of the mouse  
 Ca<sup>2+</sup>/calmodulin-dependent protein kinase IV gene.";  
 DR EMBL; M63334; AAA40865.1; ALT\_SEQ.  
 DR EMBL; M74488; AAA40845.1; ALT\_SEQ.

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RL FEBs Lett. 289:105-109(1991).  
 RN [2]  
 RP SEQUENCE OF 240-469 FROM N.A.  
 RX MEDLINE=89122027; PubMed=2536634;  
 RA Sikelala J.M., Law M.L., Kao F.-T., Hartz J.A., Wei Q., Hahn W.E.;  
 RT "Chromosomal localization of the human gene for brain  
 Ca<sup>2+</sup>/calmodulin-dependent protein kinase type IV.";  
 RL Genomics 4:21-27(1989).  
 [3]  
 RP SEQUENCE OF 315-469 FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=87104263; PubMed=3033675;  
 RR "Screening of an expression library with a ligand probe: isolation and  
 sequencing of a cDNA corresponding to a brain calmodulin-binding  
 protein.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3048-3042(1987).  
 CC -I- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING  
 PROTEIN.  
 CC -I- CATALYTIC ACTIVITY: ATP + PROTEIN = ADP + O-phosphoprotein.  
 CC -I- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL  
 NUCLEI.  
 CC -I- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE  
 TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE  
 CC SPlicing.  
 CC -I- TISSUE SPECIFICITY: BRAIN AND TESTIS.  
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC CAMK SUBFAMILY.  
 CC  
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 CC  
 DR EMBL; M16206; AAA39933.1; -;  
 DR EMBL; M64206; AAQ37564.1; -;  
 DR EMBL; J30307; AAA37566.1; -;  
 DR EMBL; X58995; CNA41741.1; -;  
 DR PIR; A29878; A28877.  
 DR PIR; S17656; S17656.  
 DR HSSP; Q63450; J106.  
 DR MGD; MGI; 80258; Camk4.  
 DR InterPro; IPR00719; Euk\_pkinese.  
 DR InterPro; IPR02290; Ser\_thr\_pkinese.  
 DR Pfam; PF00669; Pkinase; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_SR; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase; Serine/threonine\_protein\_kinase; ATP-binding;  
 KW Calmodulin-binding; Alternative splicing;  
 FT DOMAIN 306 469 CALSPERMIN.  
 FT DOMAIN 42 296 PROTEIN KINASE.  
 FT NP\_BIND 48 56 ATP (BY SIMILARITY).  
 FT BINDING 71 71 ATP (BY SIMILARITY).  
 FT ACT\_SITE 160 160 BY SIMILARITY.  
 FT DOMAIN 318 337 CALMODULIN BINDING (POTENTIAL).  
 FT CONFLICT 278 280 VLD -> CFG1 (IN REF. 2).  
 FT CONFLICT 302 302 N -> T (IN REF. 2).  
 SEQUENCE 469 AA; 52627 MW; CE1198670822F975 CRC64;  
 SQ

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Job time: 1438 sec

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